Amendments to the Specification

Please replace the paragraph at page 15, line 27 through page 16, line 6 with the following amended paragraph:

In PCR gene amplification monitoring, the detection target (the DNA or reverse transcript of RNA) is hybridized to probes that are dual-labeled at both ends with different fluorescent dyes, whose fluorescence cancels each other out. As the PCR proceeds and the Taq polymerase degrades the probe due to its 5'-3' exonuclease activity, the two fluorescent dyes become distant from each other and fluorescence is detected. Fluorescence is detected in real time. By simultaneously measuring a standard sample in which the target copy number is known, it is possible to use cycle number to determine the target copy number of the subject sample, when PCR amplification is linear (Holland, P. M. *et al.*, 1991, Proc. Natl. Acad. Sci. USA 88: 7276-7280; Livak, K. J. *et al.*, 1995, PCR Methods and Applications 4(6): 357-362; Heid, C. A. *et al.*, 1996, Genome Research 6: 986-994; Gibson, E. M. U. *et al.*, 1996, Genome Research 6: 995-1001). For example, ABI PRISM7700 (PE ~~Biosystems~~ BIOSYSTEMS) may be used for the PCR amplification monitoring method.

Please replace the paragraph at page 28, lines 16-28 with the following amended paragraph:

In a preferred embodiment of the screening method of the present invention, screening may be performed using the "two-hybrid system" (for example, "MATCHMAKER Two-Hybrid System", "Mammalian MATCHMAKER Two-Hybrid Assay Kit", "MATCHMAKER One-Hybrid System" (all of which are manufactured by ~~Clontech~~ CLONTECH), "HybriZAP Two-Hybrid Vector System" (~~Stratagene~~ STRATAGENE), and methods reported in the literature (Dalton S, and Treisman R (1992) "Characterization of SAP-1, a protein recruited by serum response factor to the c-fos serum response element." Cell 68, 597-612"). More specifically, the method of the present invention may be performed as described below, though it is not to be construed as being limited thereto, and those skilled in the art can appropriately modify the method illustrated below to achieve this invention.

Please replace the paragraph at page 30, lines 22-29 with the following amended paragraph:

In the present invention, a biosensor utilizing the phenomenon of surface plasmon resonance may also be used to detect or measure the bound compound. A biosensor utilizing surface plasmon resonance (for example, ~~BIAcore, Pharmacia~~ BIACORE, PHARMACIA) uses surface plasmon resonance signals to allow real-time observation of the interaction between the TR3 or TINUR

protein and the test compound. Therefore, biosensors such as ~~BIAcore~~ BIACORE can be used to evaluate binding between the TR3 or TINUR protein and a test compound.

Please replace the paragraph at page 36, line 26 through page 37, line 10 with the following amended paragraph:

Table 2 shows the profiles of six atopic dermatitis patients and two healthy subjects from whom blood samples were drawn. Allergen non-specific (Total IgE), mite-specific and cedar-specific IgEs were measured using the EIA method. More specifically, test sera were allowed to react with an anti-human IgE antibody-bound cap, and allergen non-specific, mite-specific or cedar-specific IgE antibodies in the sera were bound. Next, β-D-galactosidase-labeled anti-human IgE antibody and a substrate solution (4-methylumbelliferyl-β-D-galactopyranoside) were added and reacted, producing a fluorescent substance. The reaction was quenched by adding a quenching solution, and antibody concentration was determined using the fluorescence intensity of a simultaneously measured standard IgE. L-lactate dehydrogenase (LDH) was measured using the UV method (Wroblewski-La Due method). The rate of NADH decrease caused by its reaction with pyruvic acid was calculated using decreases in absorbance. L-type Wako LDH (Wako Pure Chemicals) and a 7170-type automatic analyzer (~~Hitachi~~ HITACHI) were used to measure LDH values. The number of eosinophils was measured using microscopic examination and an automatic hemocyte analyzer SE-9000 (RF/DC impedance system, Sysmex), using 2 ml of EDTA-supplemented blood as the sample.

Please replace the paragraph at page 37, line 20 through page 38, line 8 with the following amended paragraph:

A 3% dextran solution was added to whole blood drawn from a patient, and the mixture was left to stand at room temperature for 30 minutes to precipitate erythrocytes. The leukocyte fraction in the upper layer was collected, layered onto Ficoll solution (Ficoll-Paque PLUS; ~~Amersham Pharmacia~~ AMERSHAM PHARMACIA Biotech), and centrifuged at 1500 rpm for 30 minutes at room temperature. The granulocyte fraction collected in the lower layer was reacted with CD16 antibody magnetic beads at 4°C for 30 minutes. Cells were separated using Magnetic cell sorting (MACS), and cells that eluted without being trapped were used in the experiment as eosinophils.

Please replace the paragraphs at page 39, lines 4-9 with the following amended paragraphs:

One to 5 μg of this cRNA was added to a hybridization cocktail, in accordance with the Expression Analysis Technical Manual. This was placed into an array and hybridized for 16 hours at 45°C. The DNA chip used was a GeneChip^{R} HG-U95A (~~Affymetrix~~ AFFYMETRIX). GeneChip^{R} HG-U95A consists of probes comprising approximately 12,000 kinds of nucleotide sequence, derived from human cDNAs and ESTs.

Please replace the paragraph at page 40 lines 15-24 with the following amended paragraph:

Primers and TaqMan probes used in ABI7700 were designed by Primer Express (PE ~~Biosystems~~ BIOSYSTEMS) from sequence information at the National Center for Biotechnology Information (NCBI), and based on accession numbers obtained using Suite. The 5'-end of the TaqMan probe was labeled with FAM (6-carboxy-fluorescein) and the 3'-end was labeled with TAMRA (6-carboxy-N,N,N',N'-tetramethylrhodamine). The primers and probe used in the TaqMan method are shown below.

Primer 1 (5'): CCACTTTGGGAAGGAAGATGCT (SEQ ID NO: 5)

Primer 2 (3'): ACTTTCGGATGACCTCCAGAGA (SEQ ID NO: 6)

TaqMan probe: ATGTACAGCAGTTCTACGACCTGCTCTCCG (SEQ ID NO: 7)